STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _10/727,358A_

Source: _IFW16_

Date Processed by STIC: _4-5-06_

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
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1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06

IFW16

RAW SEQUENCE LISTING   DATE: 04/05/2006
PATENT APPLICATION: US/10/727,358A   TIME: 09:50:31

Input Set : A:\1216-1-006CIPSEQLISTREVISEDCEDTEXT.TXT
Output Set: N:\CRF4\04052006\J727358A.raw

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 4 <110> APPLICANT: Kolesnick, Richard N.
 5        Xing, Hong-Mei R.
 7 <120> TITLE OF INVENTION: Kinase Suppressor of Ras Inactivation
 8        for Therapy of Ras Mediated Tumorigenesis
11 <130> FILE REFERENCE: 1216-1-006CIP
13 <140> CURRENT APPLICATION NUMBER: 10/727,358A
14 <141> CURRENT FILING DATE: 2003-12-03
16 <150> PRIOR APPLICATION NUMBER: 60/384,228
17 <151> PRIOR FILING DATE: 2002-05-30
19 <150> PRIOR APPLICATION NUMBER: 60/460,023
20 <151> PRIOR FILING DATE: 2003-04-03
22 <150> PRIOR APPLICATION NUMBER: PCT/US03/16961
23 <151> PRIOR FILING DATE: 2003-05-29
25 <160> NUMBER OF SEQ ID NOS: 56
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 120
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <400> SEQUENCE: 1
35 ctgcagaagc tcatcgatat ctccatcggc agtctgcgcg ggctgcgcac caagtgctca 60
36 gtgtctaacg acctcacaca gcaggagatc cggaccctag aggcaaagct ggtgaaatac 120
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 41
41 <212> TYPE: PRT
42 <213> ORGANISM: Homo sapiens
44 <400> SEQUENCE: 2
45 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
46  1               5                  10                  15
47 Thr Lys Cys Ser Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
48              20                  25                  30
49 Leu Glu Ala Lys Leu Val Lys Tyr Ile
50          35                  40
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 19
55 <212> TYPE: DNA
56 <213> ORGANISM: Homo sapiens
58 <400> SEQUENCE: 3
59 ggcagtctgc gcgggctgc                                              19
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 18
63 <212> TYPE: DNA
64 <213> ORGANISM: Homo sapiens
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Does Not Comply
Corrected Diskette Needed
(pg. 6)

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66 <400> SEQUENCE: 4
67 tcagtgtcta acgacctc                                        18
69 <210> SEQ ID NO: 5
70 <211> LENGTH: 18
71 <212> TYPE: DNA
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 5
75 cggaccctag aggcaaag                                        18
77 <210> SEQ ID NO: 6
78 <211> LENGTH: 19
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: antisense oligonucleotide
85 <400> SEQUENCE: 6
86 cagcccgcgc agactgccg                                       19
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 18
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: antisense oligonucleotide
96 <400> SEQUENCE: 7
97 gaggtcgtta gacactga                                        18
99 <210> SEQ ID NO: 8
100 <211> LENGTH: 16
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: antisense oligonucleotide
107 <400> SEQUENCE: 8
108 ctttgcctct agggtc                                         16
110 <210> SEQ ID NO: 9
111 <211> LENGTH: 873
112 <212> TYPE: PRT
113 <213> ORGANISM: Mus musculus
115 <400> SEQUENCE: 9
116 Met Asp Arg Ala Ala Leu Arg Ala Ala Ala Met Gly Glu Lys Lys Glu
117 1               5                   10                  15
118 Gly Gly Gly Gly Gly Ala Ala Ala Asp Gly Gly Ala Gly Ala Ala Val
119             20                  25                  30
120 Ser Arg Ala Leu Gln Gln Cys Gly Gln Leu Gln Lys Leu Ile Asp Ile
121         35                  40                  45
122 Ser Ile Gly Ser Leu Arg Gly Leu Arg Thr Lys Cys Ser Val Ser Asn
123     50                  55                  60
124 Asp Leu Thr Gln Gln Glu Ile Arg Thr Leu Glu Ala Lys Leu Val Lys
125 65                  70                  75                  80
126 Tyr Ile Cys Lys Gln Gln Gln Ser Lys Leu Ser Val Thr Pro Ser Asp
127             85                  90                  95
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RAW SEQUENCE LISTING   DATE: 04/05/2006
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Input Set : A:\1216-1-006CIPSEQLISTREVISEDCEDTEXT.TXT
Output Set: N:\CRF4\04052006\J727358A.raw

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128 Arg Thr Ala Glu Leu Asn Ser Tyr Pro Arg Phe Ser Asp Trp Leu Tyr
129         100                     105                 110
130 Ile Phe Asn Val Arg Pro Glu Val Val Gln Glu Ile Pro Gln Glu Leu
131         115                     120                 125
132 Thr Leu Asp Ala Leu Leu Glu Met Asp Glu Ala Lys Ala Lys Glu Met
133         130                     135                 140
134 Leu Arg Arg Trp Gly Ala Ser Thr Glu Glu Cys Ser Arg Leu Gln Gln
135 145                 150                     155                 160
136 Ala Leu Thr Cys Leu Arg Lys Val Thr Gly Leu Gly Gly Glu His Lys
137                 165                     170                 175
138 Met Asp Ser Gly Trp Ser Ser Thr Asp Ala Arg Asp Ser Ser Leu Gly
139                 180                     185                 190
140 Pro Pro Met Asp Met Leu Ser Ser Leu Gly Arg Ala Gly Ala Ser Thr
141             195                     200                 205
142 Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala Ser Asp Ser
143         210                     215                 220
144 Pro Val Pro Gly Leu Ser Glu Gly Leu Ser Asp Ser Cys Ile Pro Leu
145 225                 230                     235                 240
146 His Thr Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser Phe Ile Thr
147                 245                     250                 255
148 Pro Pro Thr Thr Pro Gln Leu Arg Arg His Ala Lys Leu Lys Pro Pro
149             260                     265                 270
150 Arg Thr Pro Pro Pro Pro Ser Arg Lys Val Phe Gln Leu Leu Pro Ser
151         275                     280                 285
152 Phe Pro Thr Leu Thr Arg Ser Lys Ser His Glu Ser Gln Leu Gly Asn
153         290                     295                 300
154 Arg Ile Asp Asp Val Thr Pro Met Lys Phe Glu Leu Pro His Gly Ser
155 305                 310                     315                 320
156 Pro Gln Leu Val Arg Arg Asp Ile Gly Leu Ser Val Thr His Arg Phe
157                 325                     330                 335
158 Ser Thr Lys Ser Trp Leu Ser Gln Val Cys Asn Val Cys Gln Lys Ser
159             340                     345                 350
160 Met Ile Phe Gly Val Lys Cys Lys His Cys Arg Leu Lys Cys His Asn
161         355                     360                 365
162 Lys Cys Thr Lys Glu Ala Pro Ala Cys Arg Ile Thr Phe Leu Pro Leu
163         370                     375                 380
164 Ala Arg Leu Arg Arg Thr Glu Ser Val Pro Ser Asp Ile Asn Asn Pro
165 385                 390                     395                 400
166 Val Asp Arg Ala Ala Glu Pro His Phe Gly Thr Leu Pro Lys Ala Leu
167             405                     410                 415
168 Thr Lys Lys Glu His Pro Pro Ala Met Asn Leu Asp Ser Ser Ser Asn
169         420                     425                 430
170 Pro Ser Ser Thr Thr Ser Ser Thr Pro Ser Ser Pro Ala Pro Phe Leu
171         435                     440                 445
172 Thr Ser Ser Asn Pro Ser Ser Ala Thr Thr Pro Pro Asn Pro Ser Pro
173         450                     455                 460
174 Gly Gln Arg Asp Ser Arg Phe Ser Phe Pro Asp Ile Ser Ala Cys Ser
175 465                 470                     475                 480
176 Gln Ala Ala Pro Leu Ser Ser Thr Ala Asp Ser Thr Arg Leu Asp Asp
```

```
177                   485              490              495
178 Gln Pro Lys Thr Asp Val Leu Gly Val His Glu Ala Glu Ala Glu Glu
179               500              505              510
180 Pro Glu Ala Gly Lys Ser Glu Ala Glu Asp Asp Glu Glu Asp Glu Val
181           515              520              525
182 Asp Asp Leu Pro Ser Ser Arg Arg Pro Trp Arg Gly Pro Ile Ser Arg
183       530              535              540
184 Lys Ala Ser Gln Thr Ser Val Tyr Leu Gln Glu Trp Asp Ile Pro Phe
185 545               550              555              560
186 Glu Gln Val Glu Leu Gly Glu Pro Ile Gly Gln Gly Arg Trp Gly Arg
187               565              570              575
188 Val His Arg Gly Arg Trp His Gly Glu Val Ala Ile Arg Leu Leu Glu
189           580              585              590
190 Met Asp Gly His Asn Gln Asp His Leu Lys Leu Phe Lys Lys Glu Val
191           595              600              605
192 Met Asn Tyr Arg Gln Thr Arg His Glu Asn Val Val Leu Phe Met Gly
193       610              615              620
194 Ala Cys Met Asn Pro Pro His Leu Ala Ile Ile Thr Ser Phe Cys Lys
195 625               630              635              640
196 Gly Arg Thr Leu His Ser Phe Val Arg Asp Pro Lys Thr Ser Leu Asp
197               645              650              655
198 Ile Asn Lys Thr Arg Gln Ile Ala Gln Glu Ile Ile Lys Gly Met Gly
199           660              665              670
200 Tyr Leu His Ala Lys Gly Ile Val His Lys Asp Leu Lys Ser Lys Asn
201       675              680              685
202 Val Phe Tyr Asp Asn Gly Lys Val Val Ile Thr Asp Phe Gly Leu Phe
203       690              695              700
204 Gly Ile Ser Gly Val Val Arg Glu Glu Arg Arg Glu Asn Gln Leu Lys
205 705               710              715              720
206 Leu Ser His Asp Trp Leu Cys Tyr Leu Ala Pro Glu Ile Val Arg Glu
207               725              730              735
208 Met Ile Pro Gly Arg Asp Glu Asp Gln Leu Pro Phe Ser Lys Ala Ala
209           740              745              750
210 Asp Val Tyr Ala Phe Gly Thr Val Trp Tyr Glu Leu Gln Ala Arg Asp
211       755              760              765
212 Trp Pro Phe Lys His Gln Pro Ala Glu Ala Leu Ile Trp Gln Ile Gly
213       770              775              780
214 Ser Gly Glu Gly Val Arg Arg Val Leu Ala Ser Val Ser Leu Gly Lys
215 785               790              795              800
216 Glu Val Gly Glu Ile Leu Ser Ala Cys Trp Ala Phe Asp Leu Gln Glu
217               805              810              815
218 Arg Pro Ser Phe Ser Leu Leu Met Asp Met Leu Glu Arg Leu Pro Lys
219           820              825              830
220 Leu Asn Arg Arg Leu Ser His Pro Gly His Phe Trp Lys Ser Ala Asp
221       835              840              845
222 Ile Asn Ser Ser Lys Val Met Pro Arg Phe Glu Arg Phe Gly Leu Gly
223       850              855              860
224 Thr Leu Glu Ser Gly Asn Pro Lys Met
225 865               870
```

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228 <210> SEQ ID NO: 10
229 <211> LENGTH: 866
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 10
234 Met Gly Glu Lys Glu Gly Gly Gly Gly Asp Ala Ala Ala Ala Glu
235 1               5                  10                  15
236 Gly Gly Ala Gly Ala Ala Ala Ser Arg Ala Leu Gln Gln Cys Gly Gln
237           20                  25                  30
238 Leu Gln Lys Leu Ile Asp Ile Ser Ile Gly Ser Leu Arg Gly Leu Arg
239           35                  40                  45
240 Thr Lys Cys Ala Val Ser Asn Asp Leu Thr Gln Gln Glu Ile Arg Thr
241      50                  55                  60
242 Leu Glu Ala Lys Leu Val Arg Tyr Ile Cys Lys Gln Arg Gln Cys Lys
243 65                  70                  75                  80
244 Leu Ser Val Ala Pro Gly Glu Arg Thr Pro Glu Leu Asn Ser Tyr Pro
245                  85                  90                  95
246 Arg Phe Ser Asp Trp Leu Tyr Thr Phe Asn Val Arg Pro Glu Val Val
247              100                 105                 110
248 Gln Glu Ile Pro Arg Asp Leu Thr Leu Asp Ala Leu Leu Glu Met Asn
249              115                 120                 125
250 Glu Ala Lys Val Lys Glu Thr Leu Arg Arg Cys Gly Ala Ser Gly Asp
251      130                 135                 140
252 Glu Cys Gly Arg Leu Gln Tyr Ala Leu Thr Cys Leu Arg Lys Val Thr
253 145                 150                 155                 160
254 Gly Leu Gly Gly Glu His Lys Glu Asp Ser Ser Trp Ser Ser Leu Asp
255                 165                 170                 175
256 Ala Arg Arg Glu Ser Gly Ser Gly Pro Ser Thr Asp Thr Leu Ser Ala
257              180                 185                 190
258 Ala Ser Leu Pro Trp Pro Pro Gly Ser Ser Gln Leu Gly Arg Ala Gly
259              195                 200                 205
260 Asn Ser Ala Gln Gly Pro Arg Ser Ile Ser Val Ser Ala Leu Pro Ala
261      210                 215                 220
262 Ser Asp Ser Pro Thr Pro Ser Phe Ser Glu Gly Leu Ser Asp Thr Cys
263 225                 230                 235                 240
264 Ile Pro Leu His Ala Ser Gly Arg Leu Thr Pro Arg Ala Leu His Ser
265              245                 250                 255
266 Phe Ile Thr Pro Pro Thr Thr Pro Gln Leu Arg Arg His Thr Lys Leu
267              260                 265                 270
268 Lys Pro Pro Arg Thr Pro Pro Pro Ser Arg Lys Val Phe Gln Leu
269          275                 280                 285
270 Leu Pro Ser Phe Pro Thr Leu Thr Arg Arg Lys Ser His Glu Ser Gln
271      290                 295                 300
272 Leu Gly Asn Arg Ile Asp Asp Val Ser Ser Met Arg Phe Asp Leu Ser
273 305                 310                 315                 320
274 His Gly Ser Pro Gln Met Val Arg Arg Asp Ile Gly Leu Ser Val Thr
275                 325                 330                 335
276 His Arg Phe Ser Thr Lys Ser Trp Leu Ser Gln Val Cys His Val Cys
277                 340                 345                 350
```

```
<210> 23
<211> 18
<212> DNA
<213> Artificial sequence
<220>
<223>
<400> 23
atagagccca ccgcatcc                                                    18
```

pls explain

pls insert section <220> - <223>, whenever <213> Response is artificial or unknown!

See error explanation on page 7.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/05/2006
PATENT APPLICATION: US/10/727,358A   TIME: 09:50:32

Input Set : A:\1216-1-006CIPSEQLISTREVISEDCEDTEXT.TXT
Output Set: N:\CRF4\04052006\J727358A.raw

ERROR Explanation: 2

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:23

VERIFICATION SUMMARY   DATE: 04/05/2006
PATENT APPLICATION: **US/10/727,358A**   TIME: 09:50:32

Input Set : **A:\1216-1-006CIPSEQLISTREVISEDCEDTEXT.TXT**
Output Set: **N:\CRF4\04052006\J727358A.raw**

L:604 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial sequence
L:604 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial sequence
L:604 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:604